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100

RESULT :
166494/10

LOCUS	YAC ID	YAC SIZE (kb)	YAC SOURCE
166474	YAC 11	100	YAC
166475	YAC 12	100	YAC
166476	YAC 13	100	YAC
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166559	YAC 96	100	YAC

ACCESSION : 166494
 VERSION : 31:27044

KEYWORDS: Unknown.
SOURCE: Unknown.

	Unknown.
ORGANISM	Unknown.
	Unclassified

declassified.
 1. (bases) 10-7218
 Dornier, F., Schefflinger, E., and Eickro, E. (auths)
 AUTHORS
 TITLE
 Recombinant fowlpox virus
 JOURNAL
 Patent: US 5620369 A 14 SEP 1997
 FEATURES
 Location/Access

[illegible]

[illegible][illegible]

RESULT 4	
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LOCUS	AI67493
DEFINITION	Muscle cDNA sequence from strain F127-26418 of chromosome X, contig 2007432 bp.
ACCESSION	AI691493
VERSION	AI691493.16
KEYWORDS	HTG.
SOURCE	Mus musculus.
ORGANISM	Mus musculus

REFERENCE	AUTHORS	TITLE	JOURNAL
CLASS 1 (6/27/92)	Howard, P.	Direct Substitution	
	Submitted: 10 JUL 2003	Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hugh@wtsi.sanger.ac.uk	
	On Jul 11, 2002, this sequence version 149, read #1226027751		
SEQUENCE			

Genome Center
 Center for Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: hamilton@sanger.ac.uk

During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may or may not be found in the sequence corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was limited as follows: unless otherwise noted, all regions were either double stranded or sequenced with an alternative strand as indicated by high quality data (90% float ratio). In an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were generated by at least one flanking sequence or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following official sequences are used to generate primary accession numbers given in the feature table with their source databases EMBL, EMBL SWISS PROTEIN, JGI, KEGG, WPI, NCBIREF, information on the WORMPEP database can be found at <http://www.wormpep.org/>. The C. elegans genome file is available from the R61-23 Mouse PAC library (<http://www.jax.org/pac>) constructed by the group of Peter de Santis (peter@jax.org). For further details see <http://www.cbio.org/bafpac/home.htm>.

Sequence ID: BA783.6

FEATURES	LOCATION/QUALIFIERS
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	/L 42.04 01.420110090"
	/L110005.000="X"

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Query Match 12/7/97 Score 75.42 DB 97 Length 1902
 Post Local Specimen 47/887 Prod. No 9.4b.002
 Matched 2489 Unambiguous 0 Mismatches 298 1996's 0 Gaps 0

BASE COUNT 158 1 504 1 281 9 799 1

Antibiotics (Lactams)
 /codon start 1
 /product "penicillin protein PZK18.170"
 /protein_id "PZK18.170"
 /db_xref "31:18201269"
 /release_id "18201269"
 /release_id "18201269"
 /release_id "18201269"

ORIGIN

Query Match 12/7/97 Score 75.27 DB 97 Length 1902

Post Local Specimen 46/887 Prod. No 1.3b.002
 Matched 2489 Unambiguous 0 Mismatches 298 1996's 0 Gaps 0

BASE COUNT 158 1 504 1 281 9 799 1

ORIGIN

Query Match 12/7/97 Score 75.27 DB 97 Length 1902

Post Local Specimen 46/887 Prod. No 1.3b.002
 Matched 2489 Unambiguous 0 Mismatches 298 1996's 0 Gaps 0

BASE COUNT 158 1 504 1 281 9 799 1

ORIGIN

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